

SEQUENCE LISTING

<110> PEL, Herman J.
HOPPER, Sylvia

<120> GENES FROM PROPIONIBACTERIUM FREUDENREICHII
ENCODING ENZYMES INVOLVED IN VITAMIN B12 BIOSYNTHESIS

<130> 246152024900

<140> US 10/522,389

<141> 2003-07-25

<150> PCT/EP03/008216

<151> 2003-07-25

<150> EP 02255203.8

<151> 2002-07-25

<160> 17

<170> PatentIn version 3.1

<210> 1

<211> 2586

<212> DNA

<213> Propionibacterium freudenreichii

<220>

<221> CDS

<222> (1)..(2586)

<223>

<400> 1

atg	gtg	acg	gcg	acg	gct	ctt	ccg	cgg	gtg	ctc	atc	gcg	gcc	ccc	gcg	48
Met	Val	Thr	Ala	Thr	Ala	Leu	Pro	Arg	Val	Leu	Ile	Ala	Ala	Pro	Ala	
1				5					10					15		

tcc	agc	cag	gga	aag	acc	acc	gtg	gcc	atc	ggc	ctg	atg	gcg	gcc	ctg	96
Ser	Ser	Gln	Gly	Lys	Thr	Thr	Val	Ala	Ile	Gly	Leu	Met	Ala	Ala	Leu	
		20						25					30			

cgg	gcc	tcg	ggg	cgc	agc	gtg	gcc	gga	ttc	aag	gtg	ggc	ccc	gac	tac	144
Arg	Ala	Ser	Gly	Arg	Ser	Val	Ala	Gly	Phe	Lys	Val	Gly	Pro	Asp	Tyr	
		35					40					45				

atc	gat	ccg	ggc	tat	cac	gca	ctg	gcc	tgc	ggc	cgc	ccc	ggc	cgc	aac	192
Ile	Asp	Pro	Gly	Tyr	His	Ala	Leu	Ala	Cys	Gly	Arg	Pro	Gly	Arg	Asn	
	50					55				60						

ctg	gat	ccc	tat	ttg	tgc	ggg	ccc	gag	cgc	att	gcg	ccg	ttg	ttc	gcc	240
Leu	Asp	Pro	Tyr	Leu	Cys	Gly	Pro	Glu	Arg	Ile	Ala	Pro	Leu	Phe	Ala	
65				70					75					80		

cat	ggc	gcg	ctg	cat	ccc	gaa	ccc	gcg	gac	atc	tcg	gtc	gtc	gaa	ggc	288
His	Gly	Ala	Leu	His	Pro	Glu	Pro	Ala	Asp	Ile	Ser	Val	Val	Glu	Gly	
			85					90						95		

gtg	atg	ggc	atg	ttc	gac	ggc	aag	ctc	ggc	gcg	tgg	ccc	gac	ggc	acc	336
Val	Met	Gly	Met	Phe	Asp	Gly	Lys	Leu	Gly	Ala	Trp	Pro	Asp	Gly	Thr	
		100						105					110			

gat gac ccc gcc ggt ttt ggc tca tcg gcc cat atc gcc agg ctg ctc Asp Asp Pro Ala Gly Phe Gly Ser Ser Ala His Ile Ala Arg Leu Leu 115 120 125	384
gat gcc ccc gtg ctg ctc gtg gtc gac ggc tca cac agt gcc cgt acc Asp Ala Pro Val Leu Leu Val Val Asp Gly Ser His Ser Ala Arg Thr 130 135 140	432
gcc gca gcc ctg tgc cat ggc ctg gcc agc tac gat ccc cgc atc cat Ala Ala Ala Leu Cys His Gly Leu Ala Ser Tyr Asp Pro Arg Ile His 145 150 155 160	480
gtg gcc ggc gtc atc ctc aat cgg gtg atg ggt gcc cgc gtg gtc gac Val Ala Gly Val Ile Leu Asn Arg Val Met Gly Ala Arg Val Val Asp 165 170 175	528
gag atc acc cgg ggc tgc gca cgt gtc ggc ctg ccg gtg ctg ggg gct Glu Ile Thr Arg Gly Cys Ala Arg Val Gly Leu Pro Val Leu Gly Ala 180 185 190	576
ctg ccg aaa agc acg cgg gtg gcc gtg ggc tca cgc cac ctg gga ctg Leu Pro Lys Ser Thr Arg Val Ala Val Gly Ser Arg His Leu Gly Leu 195 200 205	624
gtc acg gcc gac gag cag ggt gac gcg atc ggc atc gtg cag cag gcc Val Thr Ala Asp Glu Gln Gly Asp Ala Ile Gly Ile Val Gln Gln Ala 210 215 220	672
ggt gag ctc gtc gcc gca cac ctc gac ctc gac gcc atc gcc acg atc Gly Glu Leu Val Ala Ala His Leu Asp Leu Asp Ala Ile Ala Thr Ile 225 230 235 240	720
gcc ggt ggg gcc cct gac ctg gcc gtc gat ccc tgg gat ccc gcc gca Ala Gly Gly Ala Pro Asp Leu Ala Val Asp Pro Trp Asp Pro Ala Ala 245 250 255	768
gag gtc gaa ccg gta ccg ggg cgt ccg gtc atc gcc atg gcc tcg ggt Glu Val Glu Pro Val Pro Gly Arg Pro Val Ile Ala Met Ala Ser Gly 260 265 270	816
ccc gca ttc acc ttc cgg tac acc gaa acc gca gaa ctg ctg gag gcg Pro Ala Phe Thr Phe Arg Tyr Thr Glu Thr Ala Glu Leu Leu Glu Ala 275 280 285	864
gcc ggc tgc cgg gtg acg gcc ttc gat ccg ctc acc gcc cgg ggc ctt Ala Gly Cys Arg Val Thr Ala Phe Asp Pro Leu Thr Ala Arg Gly Leu 290 295 300	912
ccg gcc gat gtg tcc ggc ctg tac ctg ggg ggt ggt ttc ccc gag gag Pro Ala Asp Val Ser Gly Leu Tyr Leu Gly Gly Gly Phe Pro Glu Glu 305 310 315 320	960
cac gcc gag gcg ctc gcc ggc aac acc tcc ctg ggc gct gaa atc gcc His Ala Glu Ala Leu Ala Gly Asn Thr Ser Leu Gly Ala Glu Ile Ala 325 330 335	1008
tca cgc gtg tcc gag ggc ctg ccg acg gtg gcc gag tgt gcg ggg ctg Ser Arg Val Ser Glu Gly Leu Pro Thr Val Ala Glu Cys Ala Gly Leu 340 345 350	1056

ctc tac ctg tgc cgc agc ctg gat gga ctg gcg atg gcc ggg gtg gtc Leu Tyr Leu Cys Arg Ser Leu Asp Gly Leu Ala Met Ala Gly Val Val 355 360 365	1104
gac gcc gac tcg tcc atg acg ccg cgc ctg acc atc ggc tac cac cac Asp Ala Asp Ser Ser Met Thr Pro Arg Leu Thr Ile Gly Tyr His His 370 375 380	1152
gcc cgc gcc gcc aac gac agc ttc ctg atg cgc gcc ggg gag cgc tat Ala Arg Ala Ala Asn Asp Ser Phe Leu Met Arg Ala Gly Glu Arg Tyr 385 390 395 400	1200
cgg gcc cat gag ttc cac cgc acc acc ctg gac acg ccc ccc tac gac Arg Ala His Glu Phe His Arg Thr Thr Leu Asp Thr Pro Pro Tyr Asp 405 410 415	1248
cgc gac ccc gga cca caa cgg ctg ggc gac caa cgg ttg gcg tgg gac Arg Asp Pro Gly Pro Gln Arg Leu Gly Asp Gln Arg Leu Ala Trp Asp 420 425 430	1296
gtg gag acc ccg acg ggg ggc aac cga ccc gag ggg gtg ctg gtc gcc Val Glu Thr Pro Thr Gly Gly Asn Arg Pro Glu Gly Val Leu Val Ala 435 440 445	1344
ccg acc ccc ggt tcc gcg ccc agc gtc cac gcc tcc tac cag cac ctg Pro Thr Pro Gly Ser Ala Pro Ser Val His Ala Ser Tyr Gln His Leu 450 455 460	1392
cac tgg gca ggg agt ccg gta ctg gcg caa cgc ttc gcc cgg gcg gcg His Trp Ala Gly Ser Pro Val Leu Ala Gln Arg Phe Ala Arg Ala Ala 465 470 475 480	1440
agc gaa tat ggg cac acc ggc cat cac tcc ccc cgg cct gcc gcc acg Ser Glu Tyr Gly His Thr Gly His His Ser Pro Arg Pro Ala Ala Thr 485 490 495	1488
acg ccg gga gat gcg ttg tcc gca gcg ccc gac ctc acc cat cac ggg Thr Pro Gly Asp Ala Leu Ser Ala Ala Pro Asp Leu Thr His His Gly 500 505 510	1536
gat cgc gat gtg ctg ccc ggc ctg gtc gac ttg gcg gtg aac gtg cgc Asp Arg Asp Val Leu Pro Gly Leu Val Asp Leu Ala Val Asn Val Arg 515 520 525	1584
gat gtg cga cct ccg gcc tgg ctc gtg gag cgc atc gtc gcc tcc agc Asp Val Arg Pro Pro Ala Trp Leu Val Glu Arg Ile Val Ala Ser Ser 530 535 540	1632
gac cag tgg gcc cac tac ccc gat cag cgc gaa gcg acc cgt gcg gtg Asp Gln Trp Ala His Tyr Pro Asp Gln Arg Glu Ala Thr Arg Ala Val 545 550 555 560	1680
gca ctg cgc cat ggc gtc aac ccc gac cag gta ctg ctc acg gcc ggg Ala Leu Arg His Gly Val Asn Pro Asp Gln Val Leu Leu Thr Ala Gly 565 570 575	1728
tcc tcg gag gcg ttc agc ctg atc gcc cac ggg ttc tcc ccg cgc tgg Ser Ser Glu Ala Phe Ser Leu Ile Ala His Gly Phe Ser Pro Arg Trp 580 585 590	1776
gcg gtc gtg gtg cat ccc cag ttc acc gaa cca gag gtg gcc ctg cgc	1824

Ala Val Val Val His Pro Gln Phe Thr Glu Pro Glu Val Ala Leu Arg	
595 600 605	
aac gcc ggg cgc ccg gtc ggc cgc ctg gtg ctc cat gcc tcg gat ggc	1872
Asn Ala Gly Arg Pro Val Gly Arg Leu Val Leu His Ala Ser Asp Gly	
610 615 620	
ttc cag ttc gat cac gaa ctg ctg gac ccc agg gcc gac atg gtg gtc	1920
Phe Gln Phe Asp His Glu Leu Leu Asp Pro Arg Ala Asp Met Val Val	
625 630 635 640	
atc ggc aat ccg acc aat ccc acc ggc gtg ctg cat tcg gcg gcg agc	1968
Ile Gly Asn Pro Thr Asn Pro Thr Gly Val Leu His Ser Ala Ala Ser	
645 650 655	
ctg cgc gcg ttg tgc cgg ccc gga cgc gtg gtg gtg gtt gac gag gca	2016
Leu Arg Ala Leu Cys Arg Pro Gly Arg Val Val Val Val Asp Glu Ala	
660 665 670	
ttc atg gac gcc gtg ccg ggc gag ccc gag agc ctc atc ggg gca cgc	2064
Phe Met Asp Ala Val Pro Gly Glu Pro Glu Ser Leu Ile Gly Ala Arg	
675 680 685	
atg gat ggc ctg ttg gtc acc cgc tcg ttc acg aag act tgg agc gtc	2112
Met Asp Gly Leu Leu Val Thr Arg Ser Phe Thr Lys Thr Trp Ser Val	
690 695 700	
ccg ggg ctg cgg atc gga tat gtg gtc ggg gat ccc gcg ctc att cgc	2160
Pro Gly Leu Arg Ile Gly Tyr Val Val Gly Asp Pro Ala Leu Ile Arg	
705 710 715 720	
gtc ctg gcg cac gaa cag ccc tgt tgg ccc atc tcc acc ccc gcc ctg	2208
Val Leu Ala His Glu Gln Pro Cys Trp Pro Ile Ser Thr Pro Ala Leu	
725 730 735	
gtc acc gcc cgc gaa tgc tcc acg cca cgc gcc gtg gag cag gcc acc	2256
Val Thr Ala Arg Glu Cys Ser Thr Pro Arg Ala Val Glu Gln Ala Thr	
740 745 750	
tca gat gcc cga cag gcg gcg cag gac cgc cga cac ctg gtg gcc cgc	2304
Ser Asp Ala Arg Gln Ala Ala Gln Asp Arg Arg His Leu Val Ala Arg	
755 760 765	
ctg gcc ggg atc ggc atc cag acc gtc ggg gag gcc agg gcc ccc ttc	2352
Leu Ala Gly Ile Gly Ile Gln Thr Val Gly Glu Ala Arg Ala Pro Phe	
770 775 780	
gtc cta gtc gac ctg cgc gcc cac ccg ccc ggt ggg ctt cgt gcg gga	2400
Val Leu Val Asp Leu Arg Ala His Pro Pro Gly Gly Leu Arg Ala Gly	
785 790 795 800	
ttg cgg acg ctc ggc ttc acc gtg cgc agc ggc gag agc ttc ccc ggc	2448
Leu Arg Thr Leu Gly Phe Thr Val Arg Ser Gly Glu Ser Phe Pro Gly	
805 810 815	
ctg ggc gcg ggc tgg ttg cgg ctc gcg gtt cgc cac ccg gac atc agc	2496
Leu Gly Ala Gly Trp Leu Arg Leu Ala Val Arg His Pro Asp Ile Ser	
820 825 830	
gac gcg ttc gtc gct gcc ctg gcc cgc acc atc gac gca ctg gac aca	2544
Asp Ala Phe Val Ala Ala Leu Ala Arg Thr Ile Asp Ala Leu Asp Thr	

835	840	845	
gcg cag cac ccc atg cga cca cca caa gga gac atc aga tga			2586
Ala Gln His Pro Met Arg Pro Pro Gln Gly Asp Ile Arg			
850	855	860	
 <210> 2			
<211> 861			
<212> PRT			
<213> Propionibacterium freudenreichii			
 <400> 2			
Met Val Thr Ala Thr Ala Leu Pro Arg Val Leu Ile Ala Ala Pro Ala			
1	5	10	15
Ser Ser Gln Gly Lys Thr Thr Val Ala Ile Gly Leu Met Ala Ala Leu			
	20	25	30
Arg Ala Ser Gly Arg Ser Val Ala Gly Phe Lys Val Gly Pro Asp Tyr			
	35	40	45
Ile Asp Pro Gly Tyr His Ala Leu Ala Cys Gly Arg Pro Gly Arg Asn			
	50	55	60
Leu Asp Pro Tyr Leu Cys Gly Pro Glu Arg Ile Ala Pro Leu Phe Ala			
	65	70	75
His Gly Ala Leu His Pro Glu Pro Ala Asp Ile Ser Val Val Glu Gly			
	85	90	95
Val Met Gly Met Phe Asp Gly Lys Leu Gly Ala Trp Pro Asp Gly Thr			
	100	105	110
Asp Asp Pro Ala Gly Phe Gly Ser Ser Ala His Ile Ala Arg Leu Leu			
	115	120	125
Asp Ala Pro Val Leu Leu Val Val Asp Gly Ser His Ser Ala Arg Thr			
	130	135	140
Ala Ala Ala Leu Cys His Gly Leu Ala Ser Tyr Asp Pro Arg Ile His			
	145	150	155
Val Ala Gly Val Ile Leu Asn Arg Val Met Gly Ala Arg Val Val Asp			
	165	170	175
Glu Ile Thr Arg Gly Cys Ala Arg Val Gly Leu Pro Val Leu Gly Ala			
	180	185	190
Leu Pro Lys Ser Thr Arg Val Ala Val Gly Ser Arg His Leu Gly Leu			
	195	200	205
Val Thr Ala Asp Glu Gln Gly Asp Ala Ile Gly Ile Val Gln Gln Ala			
	210	215	220
Gly Glu Leu Val Ala Ala His Leu Asp Leu Asp Ala Ile Ala Thr Ile			
	225	230	235
Ala Gly Gly Ala Pro Asp Leu Ala Val Asp Pro Trp Asp Pro Ala Ala			
	245	250	255

Glu Val Glu Pro Val Pro Gly Arg Pro Val Ile Ala Met Ala Ser Gly
 260 265 270
 Pro Ala Phe Thr Phe Arg Tyr Thr Glu Thr Ala Glu Leu Leu Glu Ala
 275 280 285
 Ala Gly Cys Arg Val Thr Ala Phe Asp Pro Leu Thr Ala Arg Gly Leu
 290 295 300
 Pro Ala Asp Val Ser Gly Leu Tyr Leu Gly Gly Gly Phe Pro Glu Glu
 305 310 315 320
 His Ala Glu Ala Leu Ala Gly Asn Thr Ser Leu Gly Ala Glu Ile Ala
 325 330 335
 Ser Arg Val Ser Glu Gly Leu Pro Thr Val Ala Glu Cys Ala Gly Leu
 340 345 350
 Leu Tyr Leu Cys Arg Ser Leu Asp Gly Leu Ala Met Ala Gly Val Val
 355 360 365
 Asp Ala Asp Ser Ser Met Thr Pro Arg Leu Thr Ile Gly Tyr His His
 370 375 380
 Ala Arg Ala Ala Asn Asp Ser Phe Leu Met Arg Ala Gly Glu Arg Tyr
 385 390 395 400
 Arg Ala His Glu Phe His Arg Thr Thr Leu Asp Thr Pro Pro Tyr Asp
 405 410 415
 Arg Asp Pro Gly Pro Gln Arg Leu Gly Asp Gln Arg Leu Ala Trp Asp
 420 425 430
 Val Glu Thr Pro Thr Gly Gly Asn Arg Pro Glu Gly Val Leu Val Ala
 435 440 445
 Pro Thr Pro Gly Ser Ala Pro Ser Val His Ala Ser Tyr Gln His Leu
 450 455 460
 His Trp Ala Gly Ser Pro Val Leu Ala Gln Arg Phe Ala Arg Ala Ala
 465 470 475 480
 Ser Glu Tyr Gly His Thr Gly His His Ser Pro Arg Pro Ala Ala Thr
 485 490 495
 Thr Pro Gly Asp Ala Leu Ser Ala Ala Pro Asp Leu Thr His His Gly
 500 505 510
 Asp Arg Asp Val Leu Pro Gly Leu Val Asp Leu Ala Val Asn Val Arg
 515 520 525
 Asp Val Arg Pro Pro Ala Trp Leu Val Glu Arg Ile Val Ala Ser Ser
 530 535 540
 Asp Gln Trp Ala His Tyr Pro Asp Gln Arg Glu Ala Thr Arg Ala Val
 545 550 555 560
 Ala Leu Arg His Gly Val Asn Pro Asp Gln Val Leu Leu Thr Ala Gly
 565 570 575
 Ser Ser Glu Ala Phe Ser Leu Ile Ala His Gly Phe Ser Pro Arg Trp

580					585					590					
Ala	Val	Val	Val	His	Pro	Gln	Phe	Thr	Glu	Pro	Glu	Val	Ala	Leu	Arg
	595						600					605			
Asn	Ala	Gly	Arg	Pro	Val	Gly	Arg	Leu	Val	Leu	His	Ala	Ser	Asp	Gly
	610					615					620				
Phe	Gln	Phe	Asp	His	Glu	Leu	Leu	Asp	Pro	Arg	Ala	Asp	Met	Val	Val
	625					630					635				640
Ile	Gly	Asn	Pro	Thr	Asn	Pro	Thr	Gly	Val	Leu	His	Ser	Ala	Ala	Ser
				645					650						655
Leu	Arg	Ala	Leu	Cys	Arg	Pro	Gly	Arg	Val	Val	Val	Val	Val	Asp	Glu
			660					665						670	Ala
Phe	Met	Asp	Ala	Val	Pro	Gly	Glu	Pro	Glu	Ser	Leu	Ile	Gly	Ala	Arg
		675					680						685		
Met	Asp	Gly	Leu	Leu	Val	Thr	Arg	Ser	Phe	Thr	Lys	Thr	Trp	Ser	Val
	690					695					700				
Pro	Gly	Leu	Arg	Ile	Gly	Tyr	Val	Val	Gly	Asp	Pro	Ala	Leu	Ile	Arg
	705					710					715				720
Val	Leu	Ala	His	Glu	Gln	Pro	Cys	Trp	Pro	Ile	Ser	Thr	Pro	Ala	Leu
				725					730					735	
Val	Thr	Ala	Arg	Glu	Cys	Ser	Thr	Pro	Arg	Ala	Val	Glu	Gln	Ala	Thr
			740					745					750		
Ser	Asp	Ala	Arg	Gln	Ala	Ala	Gln	Asp	Arg	Arg	His	Leu	Val	Ala	Arg
		755					760					765			
Leu	Ala	Gly	Ile	Gly	Ile	Gln	Thr	Val	Gly	Glu	Ala	Arg	Ala	Pro	Phe
		770				775					780				
Val	Leu	Val	Asp	Leu	Arg	Ala	His	Pro	Pro	Gly	Gly	Leu	Arg	Ala	Gly
	785					790					795				800
Leu	Arg	Thr	Leu	Gly	Phe	Thr	Val	Arg	Ser	Gly	Glu	Ser	Phe	Pro	Gly
				805					810					815	
Leu	Gly	Ala	Gly	Trp	Leu	Arg	Leu	Ala	Val	Arg	His	Pro	Asp	Ile	Ser
			820					825					830		
Asp	Ala	Phe	Val	Ala	Ala	Leu	Ala	Arg	Thr	Ile	Asp	Ala	Leu	Asp	Thr
		835					840					845			
Ala	Gln	His	Pro	Met	Arg	Pro	Pro	Gln	Gly	Asp	Ile	Arg			
	850					855					860				

<210> 3
 <211> 657
 <212> DNA
 <213> Propionibacterium freudenreichii

<220>
 <221> CDS

<222> (1)..(657)

<223>

<400> 3

atg gac gtt cct gac agt ccc gag tcc cga agg ctg ctc gat cag ctg	48
Met Asp Val Pro Asp Ser Pro Glu Ser Arg Arg Leu Leu Asp Gln Leu	
1 5 10 15	
tca ggc ctc ggt gcc cgg caa cgt ccg gca cga acc ctc gtc acc ggg	96
Ser Gly Leu Gly Ala Arg Gln Arg Pro Ala Arg Thr Leu Val Thr Gly	
20 25 30	
ggc gcc cgg agc ggg aag tcc agc tat gcc gag gcg ctg ctg ggg tcg	144
Gly Ala Arg Ser Gly Lys Ser Ser Tyr Ala Glu Ala Leu Leu Gly Ser	
35 40 45	
ttc gac cac gtc gac tac atc gcc acc tcg caa cgc aac cct gac gac	192
Phe Asp His Val Asp Tyr Ile Ala Thr Ser Gln Arg Asn Pro Asp Asp	
50 55 60	
ccc gag tgg atg gcc cgc atc gcc gcc cac gtc gcg cgc cgc ccg aag	240
Pro Glu Trp Met Ala Arg Ile Ala Ala His Val Ala Arg Arg Pro Lys	
65 70 75 80	
agc tgg aac acc gtg gag acc ctt gac gtg gcg cag gtg ctg tcc gac	288
Ser Trp Asn Thr Val Glu Thr Leu Asp Val Ala Gln Val Leu Ser Asp	
85 90 95	
gac ggc tcc ccc gcc ctg gtc gat tgc ctg ggc gtg tgg ctc acc cgc	336
Asp Gly Ser Pro Ala Leu Val Asp Cys Leu Gly Val Trp Leu Thr Arg	
100 105 110	
gag ctg gac gtc acc gac gcc tgg cag cac ccg gag cag gcc cgc ccc	384
Glu Leu Asp Val Thr Asp Ala Trp Gln His Pro Glu Gln Ala Arg Pro	
115 120 125	
gag ctg cag cac cgc atc gat gag ttg gcc act gcg gtc gcc ggc tcc	432
Glu Leu Gln His Arg Ile Asp Glu Leu Ala Thr Ala Val Ala Gly Ser	
130 135 140	
ccg cgc cgc gtg gtg ctg gtc acc aac gag gtc ggt tcc ggc gtg gtg	480
Pro Arg Arg Val Val Leu Val Thr Asn Glu Val Gly Ser Gly Val Val	
145 150 155 160	
ccc gcc acg cag gca ggg cgc acc ttc cgt gac tgg ctg gga atc ctc	528
Pro Ala Thr Gln Ala Gly Arg Thr Phe Arg Asp Trp Leu Gly Ile Leu	
165 170 175	
aac gcc agc gtc gcg gac gcc tgc gac gag gta ctg ctg tgc gtc gcc	576
Asn Ala Ser Val Ala Asp Ala Cys Asp Glu Val Leu Leu Cys Val Ala	
180 185 190	
gga cgg gcg ctg agc ctg cca ccg cga ccg gga ggc cct cat ggc gcc	624
Gly Arg Ala Leu Ser Leu Pro Pro Arg Pro Gly Gly Pro His Gly Ala	
195 200 205	
ggc acg gac ccc caa ccg aag gac gcg atc tga	657
Gly Thr Asp Pro Gln Pro Lys Asp Ala Ile	
210 215	

<210> 4
 <211> 218
 <212> PRT
 <213> Propionibacterium freudenreichii

<400> 4
 Met Asp Val Pro Asp Ser Pro Glu Ser Arg Arg Leu Leu Asp Gln Leu
 1 5 10 15
 Ser Gly Leu Gly Ala Arg Gln Arg Pro Ala Arg Thr Leu Val Thr Gly
 20 25 30
 Gly Ala Arg Ser Gly Lys Ser Ser Tyr Ala Glu Ala Leu Leu Gly Ser
 35 40 45
 Phe Asp His Val Asp Tyr Ile Ala Thr Ser Gln Arg Asn Pro Asp Asp
 50 55 60
 Pro Glu Trp Met Ala Arg Ile Ala Ala His Val Ala Arg Arg Pro Lys
 65 70 75 80
 Ser Trp Asn Thr Val Glu Thr Leu Asp Val Ala Gln Val Leu Ser Asp
 85 90 95
 Asp Gly Ser Pro Ala Leu Val Asp Cys Leu Gly Val Trp Leu Thr Arg
 100 105 110
 Glu Leu Asp Val Thr Asp Ala Trp Gln His Pro Glu Gln Ala Arg Pro
 115 120 125
 Glu Leu Gln His Arg Ile Asp Glu Leu Ala Thr Ala Val Ala Gly Ser
 130 135 140
 Pro Arg Arg Val Val Leu Val Thr Asn Glu Val Gly Ser Gly Val Val
 145 150 155 160
 Pro Ala Thr Gln Ala Gly Arg Thr Phe Arg Asp Trp Leu Gly Ile Leu
 165 170 175
 Asn Ala Ser Val Ala Asp Ala Cys Asp Glu Val Leu Leu Cys Val Ala
 180 185 190
 Gly Arg Ala Leu Ser Leu Pro Pro Arg Pro Gly Gly Pro His Gly Ala
 195 200 205
 Gly Thr Asp Pro Gln Pro Lys Asp Ala Ile
 210 215

<210> 5
 <211> 780
 <212> DNA
 <213> Propionibacterium freudenreichii

<220>
 <221> CDS
 <222> (1)..(780)
 <223>

<400> 5
 atg gcc acc cgc aat gga ctg ctg gct gcc tgg gga ctg ttc acg gtg 48

Met	Ala	Thr	Arg	Asn	Gly	Leu	Leu	Ala	Ala	Trp	Gly	Leu	Phe	Thr	Val		
1				5					10					15			
ctg	ccc	gca	ccc	gtg	gtg	gcc	gag	gtg	gat	gag	cga	ctc	gcc	gtg	cgg		96
Leu	Pro	Ala	Pro	Val	Val	Ala	Glu	Val	Asp	Glu	Arg	Leu	Ala	Val	Arg		
			20					25					30				
gcg	atc	gcc	tcg	atg	cgc	tgg	gtc	ggc	ctc	gga	ctg	ggc	ctg	atc	gcc		144
Ala	Ile	Ala	Ser	Met	Pro	Trp	Val	Gly	Leu	Gly	Leu	Gly	Leu	Ile	Ala		
		35					40					45					
gga	ctc	ggc	tgc	gcc	atc	gtc	acc	gtc	gcg	ggg	ggc	ggc	cag	cca	ctg		192
Gly	Leu	Gly	Cys	Ala	Ile	Val	Thr	Val	Ala	Gly	Gly	Gly	Gln	Pro	Leu		
	50					55					60						
gca	atc	gca	gca	ggc	ctg	gca	atc	ctg	gcc	ctg	tgc	acc	ggc	ttc	ctg		240
Ala	Ile	Ala	Ala	Gly	Leu	Ala	Ile	Leu	Ala	Leu	Cys	Thr	Gly	Phe	Leu		
65					70				75						80		
cac	ctc	gac	gga	ctc	gcc	gac	acc	gcc	gac	ggc	ctg	ggc	tcc	cgc	aag		288
His	Leu	Asp	Gly	Leu	Ala	Asp	Thr	Ala	Asp	Gly	Leu	Gly	Ser	Arg	Lys		
				85					90					95			
ccg	gcc	cac	gag	gcc	ctg	acc	atc	atg	cgc	caa	tca	gac	atc	ggg	ccc		336
Pro	Ala	His	Glu	Ala	Leu	Thr	Ile	Met	Arg	Gln	Ser	Asp	Ile	Gly	Pro		
			100					105					110				
atg	ggc	gtc	acc	gcc	atc	atc	ctc	gtg	ctg	gcg	ttg	gag	atc	gcg	gca		384
Met	Gly	Val	Thr	Ala	Ile	Ile	Leu	Val	Leu	Ala	Leu	Glu	Ile	Ala	Ala		
		115					120					125					
ggc	ggt	tca	gga	cac	ctt	gat	ggc	tgg	cgt	ggc	gtc	tgg	ctg	ctg	gtg		432
Gly	Gly	Ser	Gly	His	Leu	Asp	Gly	Trp	Arg	Gly	Val	Trp	Leu	Leu	Val		
	130					135					140						
aca	atg	ccc	atg	gtg	gcg	cgc	gtc	agc	gcc	ctg	tcc	gcc	acc	gga	cga		480
Thr	Met	Pro	Met	Val	Ala	Arg	Val	Ser	Ala	Leu	Ser	Ala	Thr	Gly	Arg		
145					150					155					160		
tgg	att	ccg	agc	gcc	cac	aag	aag	ggg	ttc	gga	gcg	ctc	ttc	gcc	gga		528
Trp	Ile	Pro	Ser	Ala	His	Lys	Lys	Gly	Phe	Gly	Ala	Leu	Phe	Ala	Gly		
				165				170					175				
aag	acg	cac	cct	gcg	acg	atc	gtg	gtc	gcc	tca	gtg	atc	gcc	gcg	gtg		576
Lys	Thr	His	Pro	Ala	Thr	Ile	Val	Val	Ala	Ser	Val	Ile	Ala	Ala	Val		
			180					185					190				
atc	gcc	gcg	ggc	agt	gga	tgg	ctg	ctc	ttc	ggc	tgg	cgg	gcc	gcc	ctc		624
Ile	Ala	Ala	Gly	Ser	Gly	Trp	Leu	Leu	Phe	Gly	Trp	Arg	Ala	Ala	Leu		
		195					200					205					
gtg	gcg	gtg	tgt	gcc	tgc	ctg	gcc	agc	tgg	gtc	ttc	ggc	gtg	gcg	tgg		672
Val	Ala	Val	Cys	Ala	Cys	Leu	Ala	Ser	Trp	Val	Phe	Gly	Val	Ala	Trp		
	210					215					220						
cgc	cgc	cat	atc	ctg	gcg	cgg	ctc	gga	gga	ctg	acc	ggc	gac	acc	ttc		720
Arg	Arg	His	Ile	Leu	Ala	Arg	Leu	Gly	Gly	Leu	Thr	Gly	Asp	Thr	Phe		
225					230					235					240		
ggg	tcc	ctg	gtc	gag	atg	agc	ggc	ctg	gcc	tat	ttg	ttg	acc	ctg	gca		768
Gly	Ser	Leu	Val	Glu	Met	Ser	Gly	Leu	Ala	Tyr	Leu	Leu	Thr	Leu	Ala		

245

250

255

ttg ttc gcc tga
Leu Phe Ala

780

<210> 6
<211> 259
<212> PRT
<213> *Propionibacterium freudenreichii*

<400> 6
Met Ala Thr Arg Asn Gly Leu Leu Ala Ala Trp Gly Leu Phe Thr Val
1 5 10 15
Leu Pro Ala Pro Val Val Ala Glu Val Asp Glu Arg Leu Ala Val Arg
20 25 30
Ala Ile Ala Ser Met Pro Trp Val Gly Leu Gly Leu Gly Leu Ile Ala
35 40 45
Gly Leu Gly Cys Ala Ile Val Thr Val Ala Gly Gly Gly Gln Pro Leu
50 55 60
Ala Ile Ala Ala Gly Leu Ala Ile Leu Ala Leu Cys Thr Gly Phe Leu
65 70 75 80
His Leu Asp Gly Leu Ala Asp Thr Ala Asp Gly Leu Gly Ser Arg Lys
85 90 95
Pro Ala His Glu Ala Leu Thr Ile Met Arg Gln Ser Asp Ile Gly Pro
100 105 110
Met Gly Val Thr Ala Ile Ile Leu Val Leu Ala Leu Glu Ile Ala Ala
115 120 125
Gly Gly Ser Gly His Leu Asp Gly Trp Arg Gly Val Trp Leu Leu Val
130 135 140
Thr Met Pro Met Val Ala Arg Val Ser Ala Leu Ser Ala Thr Gly Arg
145 150 155 160
Trp Ile Pro Ser Ala His Lys Lys Gly Phe Gly Ala Leu Phe Ala Gly
165 170 175
Lys Thr His Pro Ala Thr Ile Val Val Ala Ser Val Ile Ala Ala Val
180 185 190
Ile Ala Ala Gly Ser Gly Trp Leu Leu Phe Gly Trp Arg Ala Ala Leu
195 200 205
Val Ala Val Cys Ala Cys Leu Ala Ser Trp Val Phe Gly Val Ala Trp
210 215 220
Arg Arg His Ile Leu Ala Arg Leu Gly Gly Leu Thr Gly Asp Thr Phe
225 230 235 240
Gly Ser Leu Val Glu Met Ser Gly Leu Ala Tyr Leu Leu Thr Leu Ala
245 250 255

Leu Phe Ala

<210> 7
<211> 603
<212> DNA
<213> *Propionibacterium freudenreichii*

<220>
<221> CDS
<222> (1)..(603)
<223>

<400> 7
atg agc gga tcc gcg ccg cag cgc acc gag ccg acc acc gcc gaa ctg 48
Met Ser Gly Ser Ala Pro Gln Arg Thr Glu Pro Thr Thr Ala Glu Leu
1 5 10 15

cgc cac cgc ccc cga ctg atc gtg aac acc ggg aac ggc aag ggc aag 96
Arg His Arg Pro Arg Leu Ile Val Asn Thr Gly Asn Gly Lys Gly Lys
20 25 30

tcc acc gcc gca ttc ggc atg gga ctg cgg gcc tgg gcg cag ggc tgg 144
Ser Thr Ala Ala Phe Gly Met Gly Leu Arg Ala Trp Ala Gln Gly Trp
35 40 45

tcg atc ggg gtc ttc cag ttc atc aag tcg gga cgt tgg cac acc ggc 192
Ser Ile Gly Val Phe Gln Phe Ile Lys Ser Gly Arg Trp His Thr Gly
50 55 60

gag cag cag gcc tat gca cag ctc gac cag gcc cat cgg acg acc gga 240
Glu Gln Gln Ala Tyr Ala Gln Leu Asp Gln Ala His Arg Thr Thr Gly
65 70 75 80

gtc ggc gga ccg gtg gaa tgg caa tca ctc gga tcc ggc tgg tcg tgg 288
Val Gly Gly Pro Val Glu Trp Gln Ser Leu Gly Ser Gly Trp Ser Trp
85 90 95

ctg agg gcg acc gag ggc acc gac cag gca gcc atg gcg gcc gcg ggc 336
Leu Arg Ala Thr Glu Gly Thr Asp Gln Ala Ala Met Ala Ala Ala Gly
100 105 110

tgg gcc cac gtg cgc acc ctg ctc gcc gca cag acc cac cgg ctc tac 384
Trp Ala His Val Arg Thr Leu Leu Ala Ala Gln Thr His Arg Leu Tyr
115 120 125

atc ctc gac gaa ttc gcc cat gtg ctc aac aag gga tgg ctg gat gtc 432
Ile Leu Asp Glu Phe Ala His Val Leu Asn Lys Gly Trp Leu Asp Val
130 135 140

gac gag gtc gct gac gac ctg gca cat cgt ccc ggc acg caa cat gtg 480
Asp Glu Val Ala Asp Asp Leu Ala His Arg Pro Gly Thr Gln His Val
145 150 155 160

gtg atc acc gga cgc aac tgc ccc gcc gga atc atc ggg atc gcc gac 528
Val Ile Thr Gly Arg Asn Cys Pro Ala Gly Ile Ile Gly Ile Ala Asp
165 170 175

atc gtc acg tcc atg gac aac gtc aaa cat ccc ttt ggc aag gga gaa 576
Ile Val Thr Ser Met Asp Asn Val Lys His Pro Phe Gly Lys Gly Glu
180 185 190

cga gga cag gcg ggt atc gaa tgg tga
 Arg Gly Gln Ala Gly Ile Glu Trp
 195 200

603

<210> 8
 <211> 200
 <212> PRT
 <213> *Propionibacterium freudenreichii*

<400> 8
 Met Ser Gly Ser Ala Pro Gln Arg Thr Glu Pro Thr Thr Ala Glu Leu
 1 5 10 15
 Arg His Arg Pro Arg Leu Ile Val Asn Thr Gly Asn Gly Lys Gly Lys
 20 25 30
 Ser Thr Ala Ala Phe Gly Met Gly Leu Arg Ala Trp Ala Gln Gly Trp
 35 40 45
 Ser Ile Gly Val Phe Gln Phe Ile Lys Ser Gly Arg Trp His Thr Gly
 50 55 60
 Glu Gln Gln Ala Tyr Ala Gln Leu Asp Gln Ala His Arg Thr Thr Gly
 65 70 75 80
 Val Gly Gly Pro Val Glu Trp Gln Ser Leu Gly Ser Gly Trp Ser Trp
 85 90 95
 Leu Arg Ala Thr Glu Gly Thr Asp Gln Ala Ala Met Ala Ala Ala Gly
 100 105 110
 Trp Ala His Val Arg Thr Leu Leu Ala Ala Gln Thr His Arg Leu Tyr
 115 120 125
 Ile Leu Asp Glu Phe Ala His Val Leu Asn Lys Gly Trp Leu Asp Val
 130 135 140
 Asp Glu Val Ala Asp Asp Leu Ala His Arg Pro Gly Thr Gln His Val
 145 150 155 160
 Val Ile Thr Gly Arg Asn Cys Pro Ala Gly Ile Ile Gly Ile Ala Asp
 165 170 175
 Ile Val Thr Ser Met Asp Asn Val Lys His Pro Phe Gly Lys Gly Glu
 180 185 190
 Arg Gly Gln Ala Gly Ile Glu Trp
 195 200

<210> 9
 <211> 61
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 9

gggatcctct agagcatgca agcttctcga gaatcgatag atctctaagg aagctaaaat 60
g 61

<210> 10
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 10
cagtagatct cgacaaggag gaacccatga g 31

<210> 11
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 11
cgtaagatct cagtttcgga catggcagtg 30

<210> 12
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 12
caccaccaac atcgatgagg aaac 24

<210> 13
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 13
tccaattggg actcagtggg cgctg 25

<210> 14
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 14
ctgatatcaa ttggaggaca tcagatgacc cgcacgctc 39

<210> 15
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 15
ctgaattcgg ccacgtcaga tcgcgtcc

28

<210> 16
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 16
ctgatatcaa ttggaggaca tcagatgacc cgcacgtc

39

<210> 17
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 17
ctgaattccg gcggctcagg cgaacaatg

29